

601-1-098*lip*

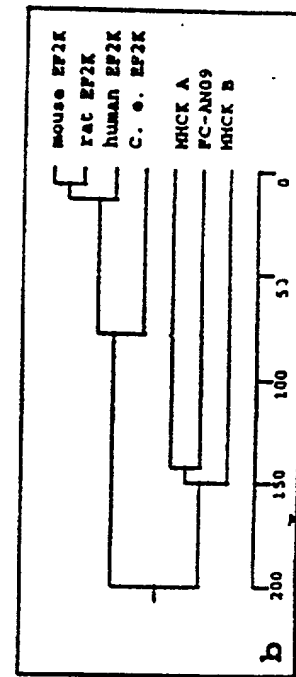
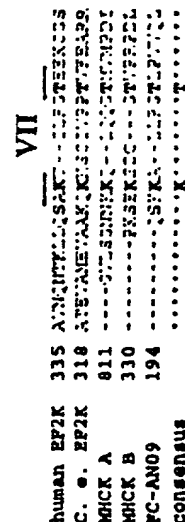


FIGURE 2

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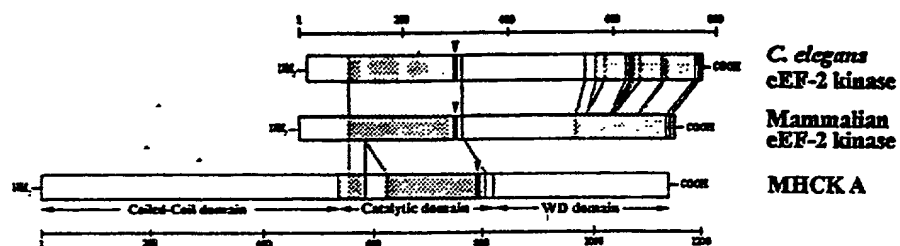
CIF

human cEF-2K	1	.....E.....QSP.....EG.....E.....	44
C. elegans cEF-2K	1	.....TIDTTNEGDNSTPAFLHASTPFLHAKNVA.....	38
mouse cEF-2K	1	.....HAEGLIFCLEGVGGRCER.....GADADPTD.....	44
human cEF-2K	45	.....F.....E.....E.....S.....R.....E.....	93
C. elegans cEF-2K	39	.....YADZVP.....SQEDVVERPND.....LLEVERELMNTT.....	79
mouse cEF-2K	45	.....HNEHVESSEVOSTYTNLTETECGS.....ZGS.....	93
human cEF-2K	94	.....E.....E.....E.....E.....E.....E.....	143
C. elegans cEF-2K	84	.....E.....E.....E.....E.....E.....E.....	139
mouse cEF-2K	93	.....E.....E.....E.....E.....E.....E.....	143
hMCK A	573	.....E.....E.....E.....E.....E.....E.....	593
human cEF-2K	144	.....E.....E.....E.....E.....E.....E.....	166
C. elegans cEF-2K	130	.....E.....E.....E.....E.....E.....E.....	150
mouse cEF-2K	143	.....E.....E.....E.....E.....E.....E.....	165
hMCK A	582	.....E.....E.....E.....E.....E.....E.....	643
human cEF-2K	167	.....E.....E.....E.....E.....E.....E.....	213
C. elegans cEF-2K	131	.....E.....E.....E.....E.....E.....E.....	204
mouse cEF-2K	144	.....E.....E.....E.....E.....E.....E.....	215
hMCK A	642	.....E.....E.....E.....E.....E.....E.....	693
human cEF-2K	213	.....E.....E.....E.....E.....E.....E.....	256
C. elegans cEF-2K	177	.....E.....E.....E.....E.....E.....E.....	239
mouse cEF-2K	213	.....E.....E.....E.....E.....E.....E.....	253
hMCK A	692	.....E.....E.....E.....E.....E.....E.....	730
human cEF-2K	287	.....E.....E.....E.....E.....E.....E.....	306
C. elegans cEF-2K	240	.....E.....E.....E.....E.....E.....E.....	289
mouse cEF-2K	256	.....E.....E.....E.....E.....E.....E.....	303
hMCK A	739	.....E.....E.....E.....E.....E.....E.....	789
human cEF-2K	307	.....E.....E.....E.....E.....E.....E.....	364
C. elegans cEF-2K	296	.....E.....E.....E.....E.....E.....E.....	339
mouse cEF-2K	306	.....E.....E.....E.....E.....E.....E.....	353
hMCK A	769	.....E.....E.....E.....E.....E.....E.....	805
human cEF-2K	353	.....E.....E.....E.....E.....E.....E.....	400
C. elegans cEF-2K	340	.....E.....E.....E.....E.....E.....E.....	386
mouse cEF-2K	354	.....E.....E.....E.....E.....E.....E.....	399
human cEF-2K	401	.....E.....E.....E.....E.....E.....E.....	449
C. elegans cEF-2K	377	.....E.....E.....E.....E.....E.....E.....	436
mouse cEF-2K	400	.....E.....E.....E.....E.....E.....E.....	440
human cEF-2K	450	.....E.....E.....E.....E.....E.....E.....	494
C. elegans cEF-2K	417	.....E.....E.....E.....E.....E.....E.....	486
mouse cEF-2K	449	.....E.....E.....E.....E.....E.....E.....	493
human cEF-2K	495	.....E.....E.....E.....E.....E.....E.....	532
C. elegans cEF-2K	487	.....E.....E.....E.....E.....E.....E.....	526
mouse cEF-2K	494	.....E.....E.....E.....E.....E.....E.....	531
human cEF-2K	533	.....E.....E.....E.....E.....E.....E.....	563
C. elegans cEF-2K	537	.....E.....E.....E.....E.....E.....E.....	566
mouse cEF-2K	532	.....E.....E.....E.....E.....E.....E.....	564
human cEF-2K	564	.....E.....E.....E.....E.....E.....E.....	596
C. elegans cEF-2K	547	.....E.....E.....E.....E.....E.....E.....	636
mouse cEF-2K	565	.....E.....E.....E.....E.....E.....E.....	595
human cEF-2K	597	.....E.....E.....E.....E.....E.....E.....	645
C. elegans cEF-2K	617	.....E.....E.....E.....E.....E.....E.....	666
mouse cEF-2K	596	.....E.....E.....E.....E.....E.....E.....	644
human cEF-2K	646	.....E.....E.....E.....E.....E.....E.....	689
C. elegans cEF-2K	647	.....E.....E.....E.....E.....E.....E.....	736
mouse cEF-2K	645	.....E.....E.....E.....E.....E.....E.....	689
human cEF-2K	699	.....E.....E.....E.....E.....E.....E.....	723
C. elegans cEF-2K	727	.....E.....E.....E.....E.....E.....E.....	760
mouse cEF-2K	689	.....E.....E.....E.....E.....E.....E.....	726

FIGURE 3

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Cif



I		II	
H. EF2K	124	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
C.e. EF2K	110	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK A	572	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK B	132	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK C	48	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
heart K	189	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
melano K	48	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
ch 4 K	1127	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
consensus		CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
III		IV	
H. EF2K	178	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
C.e. EF2K	162	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK A	653	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK B	177	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK C	89	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
heart K	249	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
melano K	108	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
ch 4 K	1173	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
consensus		CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
V		VI	
H. EF2K	252	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
C.e. EF2K	235	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK A	734	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK B	254	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK C	165	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
heart K	335	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
melano K	189	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
ch 4 K	1253	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
consensus		CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
VII		VIII	
H. EF2K	252	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
C.e. EF2K	235	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK A	734	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK B	254	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
MHCK C	165	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
heart K	335	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
melano K	189	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
ch 4 K	1253	CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET
consensus		CHENET IIMAEF G MKEF L LCHENET	CHENET IIMAEF G MKEF L LCHENET

FIGURE 5A

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CIP

1 cggggcgggg cgcgtccctc tggccagtca cccggcgagg ctgggtcgac aattatgaaa  
61 gactcgactt ctgctgctag cgctggagct gagttagttc tgagaagggt tccccgggct  
121 gtccctgttc ggtggcccggt gccaccgcct ccggagacgc tttccgatag gtggctgcag  
181 gccgcggagg tggaggagga gccgtgccc ttccggagtc cgcgccgtga ggagaatgtc  
241 ccagaaatcc tggatagaga gcactttgac caagaggagg tgtgtatata ttataccaag  
301 ctccaaagac cctcacagat gtcttcagg atgtcagatt tgtcagcaac ttgtcagatg  
361 tttctgtggc cgtttggtca agcaacatgc atgctttact gcaagtcttg ccatgaaata  
421 ctccagatgt agattgggtg aacactttaa ccaggcaata gaagaatgggt ctgtgaaaaa  
481 gcacacggag cagagcccaa cagatgctta tggagtcac aattttcaag ggggttctca  
541 ttccatagag gctaagtatg tgagactatc atatgatacc aaacctgaaa tcattctgca  
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661 catgcagaag tttgaacttc atccaagaat caagcagttg cttggaaagg gtcttattaa  
721 agctgcagt acaaccggag cttggatttt aactggagg gtcacatcag gtgtggcaaa  
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841 tggaaatagc ccatggggag tgatagaaaa cagaaatgat cttgttggga gagatgtggg  
901 tgctccttat caaaccttat tgaatccctt gagcaaattg aatgttctga ataactaca  
961 ctcccatttc atcttgggtg atgatggcac tgttggaaag tatggggcag aagtcagact  
1021 gagaagagaa cttgaaaaaa ccattaatca gcaaagaatt catgctagaa ttgggcaagg  
1081 agttcctgtg gtggctttga tatttgaagg cgggccaaat gtcactctta cagtactgga  
1141 gtaccttcag gaaagccccc cagttccagt tgttgtgtgt gaaggacag gcagagctgc  
1201 agatttacta gcctatatcc acaaacagac agaggaagga ggaaatcttc ctgatgcagc  
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3001 ctacttcaat gtcagtga caattgccat catttctttc tttgttggat ttggactaag  
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3121 attaatattac tgtcttaata taatattttg gtatgtgcgt ttgctagact ttctagccgt  
3181 aaatcaacag gcaggacctt atgtaatgat gattggaaaa atggtggcca atatgttcta  
3241 cattgtagt ataattggctc ttgtattgct tagttttggg ttcccgaaa aagcaatact

FIGURE 5B

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CIP

3301 ttatccacat gaagaacccat cttgggtctct tgctaaagat atagtttttc atccatactg  
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3541 agtgaaggca atttccaata ttgtatggaa gtatcagcgg tatcatttta ttatggctta  
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3661 ttgctgtgta tgcaaaaagaa gaaagaaaga taagacttcc gatgggcca aacttttctt  
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3781 tgatgagaaa gatgacaaat tcaattctgg gagtgaagag agaatccggg tcaacttttg  
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3961 agtagataca ttgaaaacac ttacagcca gaaagcttca gaagctagta aagtgcacaa  
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4621 atctaataga actcctgaaa acactctgaa acatgtgggt gctgctggat atagtgaatg  
4681 ttgtaagact tctacttctc ttcactcagt gcaagcagaa agctgtagta gaagagcgct  
4741 gacggaagac tctccagaag togtatttaa agcagctttg ttaccggatt ggttacgaga  
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4861 atttaagccc gttttggata caaattacta ttattcagct gtggaagaa ataacctgat  
4921 gaggttgtca cagagtattc ccttcgttcc tgtacctcca cgaggcgagc ctgtcacagt  
4981 gtaccgtctg gaggagagtt ctcccagtat actgaataac agcatgtctt catggtctca  
5041 gctaggcctc tgtgccaaaa ttgagttttt aagtaaaag gaaatgggag gtggttttacg  
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5161 ctatatcatt aagtcatttc ttoctgaggt gataaacaca tggtaagca tttataaaga  
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6061 gagagtgggt gttctctcac ctggtgcagg accattaacc aaagtcaagt cttcagattt  
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6181 ggctgaagtc ttctcagtt tgtgtcttat gataatgat ttagctctca actaggtgtt  
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6301 actgaaaacc gtttgtcttc cctctctccc tccctctttt ccctgtagta ttgaggatca  
6361 aaccaggggc ctcatgaaga ccattttcta agagacattt tatttaagaa tcaactatag  
6421 agtctatgtt tatggataca gccagttttt gttaaacaaa acctgaattg tgcaaaaggg  
6481 ttttttaaca tttatcaatg ttaagtaaaa gaaagccatg ataaataaga attaactcac  
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6661 aaaattctat aggaatgtgt caatgtgaat tctatttctg gtacttaaga aatcagttgt  
6721 tggattatcc ttatacagta tagggagatc acaatacaac tttatgcca taaaatctaa  
6781 cttaattgcc cagatatttt tgcataatta gcaacaagaa aagcttatca tttgactcaa  
6841 gttttatgct ttctctttct tttcatttcc taggtactaa ttttaatttt tatttgaag  
6901 gagcagtgtg aagcttactt gtattcaata gtgtatctca tagatacaga caaggccgca  
6961 gagataagct gttaaatagt gtttaatgtt gatgtggaga gaaagggtga ttacttaaaa  
7021 atactatacc atatacgttt tgtatatcat taaatcttta aaagaaatta aatttattct  
7081 tgtttacaaa

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KYSDVRLGEHFNQAIIEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEII  
LQLLLEKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKA AVTTGAWILTGGVNTGV  
AKHVGDALKEHASRSSRKICTIGIAPWGVNIENRNDLVGRDVPVAPYQTLNPLSKNLVNN  
LHSHFILVDDGTVGKYGAEVRLRRELEKTINQRIHARIGQGVVVALIFEGGPNVILTV  
LEYLQESPPVPVVVCEGTGRAADLLAYIHKQTEEGNLPDAAEPDIISTIKKTFNFGQSE  
AVHLEFQTMMECMKKKELITVFHIGSEDHQDIDVAILTALLKGTNASAFDQLILTAWDRV  
DIAKNHVFVYQQWLVSLEQAMLDALVMDRVSFVKLLIENGVS MHKFLTIPRLEELYNT  
KQGPTNPMLFHLIRDVKQGNLPPGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLIYNSL  
GGNNRRSGRNTSSSIPQLRKSHETFGNRADKKEKMRHNHFIKTAQPYRPKMDASMEEGKK  
KRTKDEIVDIDDPETKRFYPPLNELLIWACL MKRQVMARFLWQHGEESMAKALVACKIYR  
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CLKLAVSSRLRPFVAHTCTQMLLSDMMGR LNM RKNSWYKVILSILVPPAILMLEYKTKA  
EMSHIPQSQDAHQMTMEDSEN NFHNITEEIPMEVFKEVKILDSSDGKNEMEIHKSKKLP  
ITRKFYAFYHAPIVKFWFNTLAYLGFLMLYTFVVLVKMEQLPSVQEWIVIAIIFTYAIEK  
VREVF MSEAGKISQIKVWFSDYFNVSDTIAIISFFVGFLRFGAKWNYINAYDNHVFVA  
GRLIYCLNIIIFWYVRLD FLAVNQAGPYVMMIGKMVANMFYIVVIMALVLLSFGVPRKA  
ILYPHEEPSWSLAKDIVFHPYWMIFGEVYAYEIDVCANDSTLPTICGPGTWLTPFLQAVY  
LFVQYIIMVNLLIAFFNNVYLQVK AISNIVWKYQRYHFIMAYHEKPVLPPLIILSHIVS  
LFCCVCKRRKKDKTSDGPKLFLTEEDQKKLHDFEEQCVEMYFDEKDDKFNSGSEERIRVT  
FERVEQMSIQIKEVGDRVNYIKRSLQSLDSQIGHLQDLSALTVDTLKTLTAQKASEASKV  
HNEITRELSISKHLAQN LIDDVPVRPLWKKPSAVNTLSSSLPQGDRESNNPFLCNIFMKD  
EKDPQYNLFGQDLVPVIPQRKEFNIP EAGSSCGALFPSAVSPPELRQRRHGVEMLKIFNKN  
QKLGS SPNSSPHMSSPPTKFSVSTPSQPSCKSHLESTTKDQEPIFYKAAEGDNIEFGAFV  
GHRDSMDLQRFKETS NKIRELLSNDTPENTLKHVGAAGYSECCKTSTSLHSVQAESCRR



FIGURE 6B

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CIF

ASTEDSPEVDSKAALLPDWLRDRPSNREMPSEGGTLNGLASPFKPVLDTNYYSAVERN  
LMRLSQSIPFVPVPRGEPVTYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMGGG  
LRRAVKVLCTWSEHDILKSGHLYIISFLPEVINTWSSIYKEDTVLHLCLREIQQRAAQ  
KLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEFRKYNNNNGDEIIP  
TN  
TLEEIMLAFSHWTYETRGELLVLDLQGVGENLTDPSVIKAEKRSCEMVFSPANLG  
EDA  
IKNFRAKHHCNSCCRKLKLPDLKRNDYTPDKIIFPQDESSDLNLQSGNSTKESEAT  
NSVR  
LML

### Figure 7A

601-1-098 *cup*

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[illegible]

MSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTASLAM  
KYSDVKLGDHFNQAJEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEV  
ILQLLLKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKAAVTTGAWILTGGVNT  
GVAKHVGDALKEHASRSSRKICTIGIAPWGVNIENRNDLVGRDVPVAPYQTLNPLSKLNV  
LNNLHSHFILVDDGTGKYGAEVRLRRELEKTINQQRHARIGQGVPPVALIFEGGPNVIL  
TVLEYLQESPPVPVVVCEGTGRAADLLAYIHKQTEEGGNLPDAAEPDIISTIKKTFNFGQN  
EALHLFQTLMECMKRKELITVFHIGSDEHQDIDVAILTALLKGTNASAFDQLILTLAWDR  
VDIAKNHVFVYGQQWL VGSLEQAMLDALVMDRVAFVKLLIENGVSMMHKFLTIPRLEEL  
YNTKQGPTNPMLFHLVRDVKQGNLPPGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLIY  
NSLGGNNRRSGRNTSSSTPQLRKSHESFGNRADKKEKMRHNFHFKTAQPYRPKIDTVME  
EGKKKRTKDEIVDIDDPETKRFPYPLNELLIWACLMKRQVMARFLWQHGEESMAKALV  
ACKIYRSMAYEAKQSDLVDDTSEELKQYSNDFGQLAVELLEQSFRQDETMAMKLLTYE  
LKNWSNSTCLKLAVAAKHRDFIAHTCSQMLLTDMWMGRLRMKRNPLGLKVLVPPAI  
LLEYKTKAEMSHIPQSQDAHQMTMDDSENNFQNTTEEIPMEVFKEVRILDSNEGKNEM  
EIQMKSSKLPITRKFYAFYHAPIVKFWFNTLAYLGFLMLYTFVVLVQMEQLPSVQEWIVI  
AYIFTYAIEKVREIFMSEAGKVNQKIKVWFSDYFNISDTIAIISFFIGFGLRFGAKWNFANA  
YDNHVFVAGRLIYCLNIIFWYVRLLDFLAVNQAGPYVMMIGKMVANMFYIVVIMALV  
LLSFGVPRKAILYPHEAPSWTLAKDIVFHPYWMIFGEVYAYEIDVCANDSVIPQICGPGT  
WLTPLQAVYLFVQYIIMVNLLIAFFNNVYLQVKAINIVWKYQRYHFIMAYHEKPVLP  
PLIILSHIVSLFCCICKRRKKDKTSDGPKLFLTEEDQKKLHDFEEQCVEMYFNEKDDKFHS  
GSEERIRVTFERVEQMCIQIKEVGDRVNYIKRSLQSLDSQIGHLQDLSALTVDTLKTLTAQ  
KASEASKVHNEITRELSISKHLAQNLIDDGPVRPSVWKKHGVVNTLSSSLPQGDLESNNP  
FHCNILMKDDKDPQCNIFGQDLPAVPQRKEFNFEAGSSSGALFPSAVSPPELRQRLHGV  
ELLKIFNKNQKLGSSSTSIPHLSSPPTKFFVSTPSQPSCKSHLETGTDQETVCSKATEGDN  
TEFGAFVGHRSMDLQRFKETSNIKILSNNNTSENTLKRVSLSLAGFTDCHRTSIPVHSKQ  
EKISRRPSTEDTHEVDSKAALIPVWLQDRPSNREMPSEEGTLNGLTSPFKPAMDTNYYYSS  
AVERNLMRLSQSIPFTPVPPRGEPVTVYRLEESSPNILNNSMSSWSQLGLCAKIEFLSKE  
EMGGGLRRAVKVQCTWSEHDILKSGHLYIISFLPEVVNTWSSIYKEDTVLHLCLEIQQ  
QRAAQKLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEF  
RKYNNNGDEIIPNTLEEIMLAFSHWTYETRGELLVLDLQGVGENLTDPSVIKAEK  
SCDMVFGPANLGEDAIKNFRAKHHHCNSCCRKLKLPDLKRNDYTPDKIIFPQDEPSDLNLQ  
PGNSTKESESTNSVRLML

Figure 7B

**Figure 8A**

ESAEPLTQSDKRETSHTTAAATGRSSHADARECAISTQAEQEAKTLOTSTDSVSKEGNTNCKGEGMQVN  
TLFETSQVPDWSDPPQVQVQETVRETISCQMPAFSEPAGEESPFTGTTISFNLGGVHKENASLAQHSEV  
KPCTCGPQEEKQDRDGNIPDNFREDLKYEQISEANDETMSPGVFSRHLPKDARADFREPVAVSVASPEP  
TDTALTLENVCDEPRDREAVCAMECFEASDQGTCTDIDSLVGTVPVDNYSPOEICSVDTELAEGQNKVSD  
LCSSNDKTLEVFFQTQVSETSVSTCKSSKDGNSVMSPLFISTFTLNISHTASEGATGENLAKVEKSTYPLAS  
TVHAGQEQSPSNSGGLDETQLLSENNPLVQFKEGDKSPSPAADTTATPASYSSIVSFPWEKPTTLTAN  
NECFQATRETVTIATEVHPAKYLAVSIPEDKHAGGTEERFPRASHEKVSQFPSQVQVDHILSGATIKSTKEL  
LCRAPSPGVPHHVLQLPEGEGFCNSPLQVDNLSGDKSQTVDRADFRSYEENFQERGSETKQGVQQQSL  
SQQGLSAPDFQQSLPTTSAAQEERNLVPTAPSPASSREGAGQRSWGTRVSVVAETAAGEEDSQALSNVPS  
LSDILLEESKEYRPGNWEAGNKLKIITLEASASEIWPPRQLTNSEKASDGLIIPDKVWAVPDSLKADAVV  
PELAPSEIAALAHSPEDAESALADRESHKGEEPTISVHWRSLSSRGFSQPRLLESSVDPVDEKELSVTDSLS  
AASETGGKENVNVNSQDQEEKQLKMDHTAFFKKFLTCPKILESSVDPIDEISVIEYTRAGKPEPSETTPQGA  
REGGQNDGNMGHEAEIQSAILQVPCLOQTILSENRISSQEGSMKQEAEOIQPEEAKTAIWQVLQPSGEG  
ERIPSGCSIGQIQESSDGLGEAEQSKKDKAELISPTSSCLPIMTHSSLGVDTHNSTGQIHDVPENDIVEP  
RKROYVFPVSQKRGTIENERGKPLPSSPDLTRFPCTSSPEGNVTDFLISHKMEEPKIEVLQIGETKPPSSSSSS  
AKTLAFISGERELEKAPKLLQDPCQKGTLCAGKKSREKESLEARAGKSPGTLTAVTGSEEVKRKPEAPGS  
GHLAEGVKKKILSRVAALRLKLEKENIRKNSAFLKMPKLETSLSHTEEKQDPKKPSCCKREGRAPVLLK  
KIQAEMFPEHSGNVKLSQFAEIHEDSTICWTKDSKIAQVQRSAGDNSTVSFAIVQASPKDQGLYYCCIK  
NSYGKVTAEFNLTAEVLKQLSSRQDTKGCEEIEFSQLIFKEDFLHDSYFGGRLRGQIATEELHFGEGVHRK  
AFRSTVMHGLMPVFKPGHACVLKVHNAIAYGTRNDELQIRNYKLAQECYVQNTARYYAKIYAAEAQ  
PLEGFGEVPEIPIFLHRPENNIPYATVEEELIGEFVKYSIRDGKEINFLRRESEAGQKCCTFQHWVYQKTS  
CLLVTDMMQGVGMKLTDVGIATLAKGYKGFKGNCSCMTFIDQFKALHQCNKYCKMLGLKSLQNNNQKQK  
QPSIGKSKVQTNMTVKKAGPETPGEKKT

Figure 8B

1 atgtccaga aatcctggat taaaggagta ttgacaaga gagaatgtag cacaatcata  
 61 cccagctcaa aaaatcctca cagatgtact ccagatgccc aagtctgcca gaatttaac  
 121 aggtgttact gtggccgact gattggagac catgctggga tagattatc ctggaccalc  
 181 tcagctgcca agggtaaaga aagtgaaca tggctgttg aaaagcacac aacgaaaagc  
 241 ccaacagata ctittggcac gattaattc caagatggag agcacacca tcatgccaa  
 301 tatattagaa ctcttatga taaaaactg gatcatctg tacatttaat gttgaagag  
 361 tggaaaatgg aactgccaa gcttgatc tcagtcctg gggccacca gaatttact  
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 481 ggagcgtgga taataactga aggcataat acagtgtcca agcatgtg ggaagcctg  
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 661 gataccccc tcagcaagct cacaacact aacagcatg actgcactt catctgtct  
 721 gatgatggga cgtgggcaa gtatggaat gaaatgaagc tcagaagaa cctggagaag  
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 1321 cgggtggtt ttgtgaagct cttaalagaa taaggatga acctccatg ctitttacc  
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 1441 catctgtcc aagatgtga acagataac ctcttctcag gctaccgat aaccttgat  
 1501 gacattggat tagtagtaga atacctatt gtagagcat atcgagcaa ctacactaga  
 1561 aaacattca gagccctcta caaacctc tacagaaaat aacagacca gagacactcc  
 1621 tcaggaaaata gaaatgagtc tcagaaaagt acgtgcact cccagttat tagaactgca  
 1681 cagccataca aattcaagga aaagtctata gtcctcata aatcaaggaa gaagtcaaaa  
 1741 gaacaaaatg tatcagatga ccttgagctt actggcttt ttaccctta caatgacctg  
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 3421 cagtgcgtg aaaaatactt ccatgagaag atggaagat tgaatttag ttgtaggaa  
 3481 cgaatccgag tgacatcaga aagggttaca gagatgtact tccagtgaa agaaatgaat  
 3541 gaaaaggtgt ctttataaa ggaactctta ctgtcttgg acagccaggt gggacacctg  
 3601 caggatctct ctgcccgtac tttgatacc ctgaaagtc tttctgtg tgacatttg  
 3661 caagaggatg aggtctctt ggccaagaga aagcattcta ctgcaaaa acttcccac  
 3721 agctggagca atgtatctg tcagaggtt ctaggcagca tggagatgc tggagagaag  
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 3841 cccccagag tgacagaggg ggcactctt gagattacaa acagtaaa agaggtctca  
 3901 aattgaagaa atgaccagga aagcgaagaa acacaaagta gtatagtggt tctgtgggtg  
 3961 tctctaaca ggcaagcaca ctcaagatg ggccagttt tctgtgcc ctctaacta

Figure 9A

4021 aagcaggttc cttttcagc agaaactgtc ttgcctctgt ccagaccctc tgtgccagat  
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 7981 attctacaag tcagtaagg aacaattgtt actcacctca gtgtgact caactatgga

Figure 9A

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8041 aagaggcaga gttgcttgc ccaattgeca aactaaagac atcagttcat tggtaasata  
8101 ttgttacct ggaatggaac tgaagagca atacatttg atticaatt tcaaaaaa

**Figure 9A**

8041 aagaggcaga gttgcttgc ccaattgeca aactaaagac atcagttcat tggtaasata  
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## Human kidney kinase

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 PYNDLLVWAVLMKRQKMAMFFWQHGE EATVKA VIACILYRAMAHEAKESHMVDDAS  
 EELKNYSKQFGQLALDLEKAFKQNERMAMTLLTYELRNWSNSTCLKLAVSGGLRPV  
 SHTCTQMLLTDMWMGRLKMRKNSWLKIIISILPPTILTLEFKSKAEMSHVPQSQDFQFM  
 WYYSQDNASSSKESASVKEYDLERGHDEKLDENQHFGLSEGHQHLPWTRKVYEFYSAP  
 IVKFWFYTMAYLAFLMLFTYTVLVEMQPQPSVQEWLVSIYIFTNAIEVVREVSISEPGKF  
 TQKVKVWISEYWNLTETVAIGLFSAGFVLRWGDPPFHTAGRLIYCIDIIFWFSRLLDFFA  
 VNQHAGPYVTMIAKMTANMFYIVIIMAIVLLSFGVARKAILSPKEPPSWSLARDIVFEPY  
 WMIYGEVYAGEIDVCSSQSPCPPGSFLT PFLQAVYLFVQYIIMVNLLIAFFNNVYLDMESI  
 SNNLWKYNYRYIMTYHEKPWLPPPLILLSHVGLLLRRLCCHRAPHDQEEGDVGLKLY  
 LSKEDLKKLHDFEEQCVEKYFHEKMEDVNCSCEERIRVTSE RVTEMYFQLKEMNEKVS  
 FIKDSL LSLDSQVGH LQDLSALTVD TLKVL SAVDTLQED EALLAKRKHSTCKKLPHSWS  
 NVICAEVLGSMEIAGEKKYQYYSMPSSLLRSLAGGRHPPRVQRGALLEITNSKREATNV  
 RNDQERQETQSSIVVSGVSPNRQAHSKYGQFLLVPSNLKRVPFSAETVLP LSRPSVPDVL  
 ATEQDIQTEVLVHLTGQTPVVSDWASVDEPKEKHEPIAHL LDGQDKAEQVLP LTL SCTPE  
 PMTMSSPLSQAKIMQTGGGYVNWAFSEGDETGVFSIKKKWQTCLPSTCDS DSSRSEQHQ  
 KQAQDSSLSDNSTRSAQSSECSEVGPWLQPN TSFWINPLRRYRPFARSHSFRFHKEEKL M  
 KICKIKNLSGSSEIGQGA WVKAKMLTKDRRLSKKKKNTQGLQVPIITVNACSQSDQLNP  
 EPGENSISEEEYSKNWFTVSKFSHTGVEPYIHQKMKTK EIGQCAIQISDY LKQSQEDLSKN  
 SLWNSRSTNLNRNSLLKSSIGVDKISASLKSPQEPHHHYS AIERNLMLRLSQTIPFTPVQL  
 FAGEEITVYRLEESSPLNLDKSMSSWSQRGRAAMIQVLSREEMDGGLRKAMRVVSTWS  
 EDDILKPGQVFIVKSFLPEVVRTWHKIFQESTVLHLCLREIQQQRAAQKLIYTFNQVKPQ  
 TIPYTPRFLEVFLIYCHSANQWL TIEKYMTGEFRKYNNNNGDEITPTNTLEELMLAFSHW  
 TYEYTRGELLVLDLQGVGENLTDPSVIKPEVKQSRGMVFGPANLGEDAIRNFI AKHHCN  
 SCCRKLKLPDLKRNDYSPERINSTFGLEIKIESAEPPARETGRNSPEDDMQL

Figure 9B

GTATCAGGACTAGCCCATTTCCCCCTCTGCTGAGAAATGGAGGCCGAAGTGATCTAGAAAGTTAAATTGAGCCCTTAATCTATGCTAGTTACTGGGGTGTGTGGGGGAGACAGGAGAGATCCACAGGGGTTCGGCCCTCCACGGACTCAGGTCATAATGAGAGTGGCTTGGCTTGTCTATGTGTGGGCCAACACAGCCA CTGGGAGGCAAGAGGGTCAAGTACAGGCTGTGCCAGAAAGAGGGCTGTCTTGGCTCCCTGCTCCCGGCTTAGCCCAAGCTAGCCACGGGTGGACTGAC CTGGTCTCCCTGGCCCGCCAGGCTCTGTGGACCCCTCATATGCCACACGGGACTCTCCAGCGCGGCTCTCCAGCGCGGCTCCGGGAGCTCCAGGAAGCTCCACGAAGGGGCC TGTCTCCATGACCAGGACACCCGCTTCTCTCCGAGGCTCCCGGGCTCTCCAGCGCGTCTCAAGCCGCTCCCGGCTCGGCCAGCGCAGGGAGGACAGCAGCAGGTG CCGAGCCGCTTGGCGGGACATGGGCCCCGCGCCCCCGGCTCTCAAGCCGCTCCAGCCGCTCCAGCGCGTCCAGCGCTACCTGTCTCAGCGTTCAGCGCTTATCAAGCTCAACCTGGTGT GTACAGCGACGTCAGGTTTCACTGTCTACAGGATACCCAGAGCCAGAGGTGACTGTGTACAAGGATGATACGGAGCTGGACGCTACTGTGGCTTCTGTGTCTGTTCC AAAAAATGAGATCACTCATCAGGGCAACCCGACACACTGCACTGTACAGGTGTGAGAAAGATGCCGCCATCTACAGGCTCTGCCAGAACAGCAAGG CATGTGTCTCTCAGGGTCTGTGAGGTGGGACCATGTACTGTAGTACAAAGTCCACAGCTGTGTGTGCCAAGTTGAAGCGCAAGGCTGGGCAAGGCTG CCGAGATGTGAGAGACTGGAAAGCAGAGAGGCGTGTGGGGAGGTGCACACTTGGCGAAAGCTCAGCCCCGACCGCTTCCAGCGAAAGCGGCGATTGA CGGGGCTCAACGCGCGGCCCTCGGTCCCTACCAAGGAGCCTACCAAGGAGCTTGGCGGGTGGCAGGCTTGGCAGGAGGAGAGACTGAGACTGCTCAGCACTCAGCACTCTGACATCATCTG TTGGGCTGATCAACAGTTTGTCTCTGGAGAACTGACCAACCGGGAGGCTGCCCCGAGATGGAGAGGACGAGACGATGGCTTGTCTGACATCATCTG TGACGCCATGGAGCTGGGCCCTCAGAGAGCCCTAAAGAGGAGAGTGGGCCAAGAAAGAAAGATGAGGAATCCAAAGCAAGGCTTCGGGAAGCCAGA GTTACAGAAAGCAGCCAAAGCCGCTTCTCAGAAAAGTGTCTCCAGCTCAGCAGAGCTGACTCTGTGGGACTCAGGGGCCCTGGGGCTGGAGCAGG TTACAGACCCAGCCAGGACAGGCTGCACGGGGCTTGGTCTCTTGAGACATAGTATCCAGGAAGCCAGGCTTGTCTGTGGGCACTCCAGACAAAGGCCAG AAGGCCCTGGCCAGCCAGCCAGGCGCAGGAAGTATTTCTCTTTGAAAGGACATGATACCTTGAGAACACCCAGGCACTAGGCTCTTGGGGAAGAGGACCCCA GAACCTTGAGTGTCCGGGCGCTGGGAGAGTCCCAAGGGGAGGACCCCTCAGGGCTAGAGAGCAGGGGTGGCTGGCGTCTTGGGCAAGCACAACACTCTC TGACCCCCAGCGCACTAGGCTTTCAACAGAAAGATTTGCCCTTCCAAAGCCCAAGAGAGGCCACCACTGACAGCAAGCCCATTTCTTCTGTAGTCAAG CTCAGAAATGGGGGCGCCAGACTAGGAAAGGCCCACTCAGGCTCTGTGACGGTGGCGAGCGCCCTGCCGCGGAGACATGGCACCCGGGACAGCAGC TTGCAGGGGCAAGCGCCACAGGACTCCAGGACAGTCTTGAAATGCCAGACCAACCGGCTCTACCATCTGGGCGACAGCACTGTGATGTAGCCTTCAAT TGGGCTTAGCATTCGGGAAGTCAAGGTATCATTTGAACCCATGGATATGGAACCCAGGAGATGGGAACATCTGTCTAACAGAGAACTGGAAGCAAGTAAATGTGACGGCAGATGGGAAGATACAAGTGGATGGAAGCACAGGAGATGGAACACAGCACGCCAGGAGACAGTGCAGATAGGAAGACGCAAGTGGAT GCTGGGACACAAGAAAGCAAGAGGCCACAGTCAGACAGGATGTCACAGAGGGCATGATGACACAGGAAGGCGAGACACAGCTAGAAACAACACAGGCA GTGTAAGAAATACAGAAAGACGGAAGCCAGGACATAGGGCACACAGGAAGATGCAAGGAGATGCAAGGAGATGCAAGGAGACAGGGATGCAAGGAGAGAGGGGAC GCATCAGAGGGGAGCGGCCACAGCATGGAAGGTGACTGTAGCAAGAGTGGCAACAGGCTCGGCCCACTCCAGACCCCAACTCCCACTCAG CCGTCTCTAGACTCTCTGAATATTTGAATGTTTGTACAGACCCCAAGAGGTTCTTTTCCCAAAAAAACCCTGTTGCCCTGCCAGATGTGAGGAGGCAAGTAG TAAACGCTCCAGGAACCATGAGCAAACTGTGCTGGTCCCCTGTCAAGGAACCTATGCTCCAGCACAGCCGCCCCATGAGGGGAGTGTGGAGCAGGTGGGA GGAGAGAGATGCGAGGGCCACAGTCATCAGGCCCATGTCAGAGCCCATGCAAGGCCAAGCAGGAGGACAGCCGTTCCAGTGCCCCAAGGAGCGGCCAGGGGAGTGCCT GTATGATCAGGGTGGCTGTCTCTAGCTGTGCTCAGCAGGATACCCAGATCCCTCTCTCTCTGAACTGGCTGACGCTTCCCAAGAGCGGGGCCGT CCACTCAGGACTCCCAAGAACCATGGCCACCATGAGGGGGCTCGGCCAGGTACCGCAGGTACCGGAGTGTGGAGGGCGGACCCAGCTGCACTGGGGCTGGGAGCCC CCCTGGCTCTATAGATTCCTGAAAGAACTCTGCTGCTGAAGCTGTCCAGCACAGACAGAAAGTGGAGCAGGGGAGAGTCCCAAGTGGGGGCGACGCCAC CGGAGGTCTGTGGCTCAGCCACTGTGACACCCACTGTGGAAGTGGCTGGCTTAGTCCCCGACATCGAGGGCATCTCTGGAGCTGTGGAGAACACCAACCT GTGACAGAGTGCAGACACTGTGTGAGCCCTGTACTCCCCCGCTCACCGGCTTGGAGGCTGTGAGGTGACGCTTGGCGCCAGGCCCTTGTGCTGTG CCGAGGCTCTGGGTCTGTCCAGTCTCCCTCACTGTCCCTGCCATTTGTGTAGAGGAGACCTTGGCTGGCTCAGAAAGGACCACTGTGAGGTGAAG GAGAGGTTTCCCTGTAGGGGCTGGCTCTCAGGAGAGACGATGCTGTGTCGATGGGAGGGGTGGGAGGCGGCTGGGACGCGCCCTGGACAGGGG CCTCAGCAGAGAGCATAGCCAGGAGCCCTCCCAAGAGGAGAAAGTTCCAGGGGAGGCTCTGACAGGCTCCCGGACGCTACACCTTAGGAACTGGCTTAGG

GGCCCCGAGGAAGAGATTCTCCCTAAGTCAGACGACGAGACGGGGAGGCAACACACCTGAAGAAAGGAGAGCCACAGGTTTCCCCCGGGGGCCCC  
AGGAAAGAGCTGGTGCCTCCAGGACTCCAGGGGGGAGAGACGCTCCCTACCGCAGGGCAGAAAGCGAGCATGCTGGAGGTGCCTCGGGCAGAGAG  
AGGAGCTGGCGGCAGGAGACTGGGCCCCAGCCCAAGCGCGGTCTGGACACAGAGGTGGCTTGGATGAAGGCAAGCAGAGAGACACTGGCCAAAGCCCAAG  
GGAAGGCAAGCAAGACTGCTGAAGCCCCACAGGTGATCCGGAAGATTCGGTGGAGCAGATTCTCTGATGCTCCGTGAGCTGAAGCTGAGGTGGCAGCTTTCTCAA  
CACTTCTTAGACTCATGTTGACATGGGCCAAGGATCAGCGCCCATGGCGAGGTGGCAGGACGCGCAGGGGTAGCGAGGCGCGCGGCTTGGCCATTTCTGTC  
TAGGCTTCCCGGTAGCTCGGGTGTGATTCGGTGCACCATCCAAATGACACGGCTCGGCCCTCACCGACTCTGCCCTCAGCCCTCAGGTGTGTCAGGATTCAT  
CTCCAGAGAAGAAAGGTGAAGTTGGAGAAGAGATTGAGATGACCCCTATGGTGTTCGTAAGGGTCTGGCTGACTCTGGCTGCTGGGGGAGACAAGCTCTTTGGGC  
GACTGTTAAGCAGGAGCTCCGAGGGGTGGATATGGGTGTGGCTTCGGAAGGCCCTCCAGGCCAAGGTGATCTACGGCTGGAAACCATCTCCGAGTCCGGGC  
CCGACGTCATCAAGGTGTCCAGGCTGTGTGTGGGCCACGACGTGAGACTTCTGTGGGCAGAAACTACGACTCACCATCCAGGTGTGCAAGATC  
CAGAAACATGATCGGAGTACTGCAAAATCTTCGACAGAGAACCGCGGGCGCGCTGGCTTGTGGGAGGTGCCCTGAGATCATCCCACTGTATCTGATCTACCCG  
CCTGCAAAACGATATCCCATATGCTACCCCTGGAGGAAGACCTGGCAAGCCCTGGAGTCTACTGTCTCGGAAATGGGGCTGTGCTGAGGCTCCGACAGCATCT  
CTGAGGGCCATGCAAAATGCCAGACTTCCAAACACTGGCTGTATCAGTGGACAAATGGCAGCTTCTTGTACACAGACTTGGCAGGGGTGTGACTGGAAG  
ATGACTGATGTGCAGATTGCTACCAAACTCCGAGGATACAGAGGCTCAAGGAAGCTGTCTCTGCCCCCTGGACCGGTCTGCCCTCCACACCATGTGCAAT  
GGCTTACTGTGAGCTGTGGGCTGACACCTCTCAAGGGCCGAGGGGCCAACCCCAAGCAAGCAAGGCTCTAAGAGTCCATCTGTGGCAGGAAAGG  
CTCCCACTGTGCTCAGCCCAAGAAAGGCTCCCTAGTCTCAGGCCACCCGGAAGAGTGTCTCCAAAGTTCCAAAGGCCACCCCTCAGGCTCAGGCCCATGAGCCAGTA  
CACCACCTGATGTTGGGACAGCTTCCCAACCAAGAGGAGGCTCCAAAGGCCAGGGCATGGGTAGCTCTGACAGAGGCTGGGGGCTCCACCCACGACGACGTA  
CCCAACGAGGACAGCTTGAATGAGTGGAGACTTCCAAATATGAACTAACTGGAGAAAGTGCACGAAGGAGACCACTTGGGGACCTCTCTGAGCAGGCT  
CTCGTGAATCAGCTGTCATCAGATGGCTTTGGTGCAITGGCACATAGCCCACTGGCCCTCTCTGTGTGCCACTGTCAACCCAGGGCTCCCGGGCTCAAGAGTCCCC  
ACCTCCGAGTGCCTGGCAACCTAGGCCCTCTTGAAAGTTACACTTGGCCACTGCTGGAGGCTCCCTGAGTCTCTGCATGAGTCTGCAACCCCAAGCCCTTGGC  
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AGACTTCTCTGCTGTGGCTTGGCTGTGACTCTCAGGTTATCTTCTCTCCAGCTACTTTCGCTCAGCTATCTCTGCACATTAACCATCTCTGAGCC  
AGATGGGCTCAGGGCCCTCCAGAGCCTGTCAITGCTTGTGAGTGGCTTGTAGTGTGTCACTCTCCCTCTCACTCACTCGCTGTCTCCCATGCTCTC  
CTGTGACCCCTTGCCATCCCTGTCTTGGGCCCAGCTGCAGCTGTGCTGCCCTTCACTGCTCTCTCTCCCACTCTCTCGGGCTCTTGTCTCATGAGGTGAGAGCTGGTG  
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TCAACAGGAGGTGAGGGCTAGGTCCCTTCCCATTTGGGAGTACATTTGGTGTCTTAGGAGGTGCACTTCCATGCATCTGGGTGAGGGGAGTCTGT  
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AGAGACTCCCTCTCTGGAGGCTGGGTAGGTCTGCAGCTAGCCTACTCCCTTTGGAAITGCAATAAGAGCAGATTTGTGTGCCCTGCTTGGCCCTCATCTGGT  
GTGGTTGGAGGTCTGTGAGTCAAGTCCCCCTCTCCAGGCAAGCTCTCTGAGGGCAATCTGTAGTCCAGGCCCACTGGAAANAATGAATCTATATTTTGGTTCC  
TGGAACGAAGTTCAGTCGACGCTTCTGTGGCCACAGAAAGACAGCTTGTGCTGTCTGCAACACTGAGCTGTGGTGTACCCCTTAGCAGGGTGTCTCTGGGAC  
TTACGGCTTTTGAATTTGCTCTCATTCAGAAGAGGAACAACAAGGAAGCAACCCAGGAAGCAAGCAGAGAGCTGGGGCTTGGAAACGCCCTGTCTCTGGC  
TCAGACGAACCAAGCCAGGAGCCCAAGCAACCTGCTCTCAGCTACTTGTGACCAATTCCTGCTCTCAAGCTGCAGAGAGGTTTCAATCCACACCCACCC  
CCGAACCTCCCTTGCCTAAACATTTCCCTCTATGGTAACATCTCTACCTCTCTGCTCAGGTGACTCCACATCTTCTGCCCCAGTGTGTCCCCAC  
TCTCTCCAGGCTGTATACCCAGATTACTTTGGTGAACTGAAAAA

MEVAWL VYVLGQQPLARQEGGQSRLVPGRGLVLWPLGLPRSSPSWPAVDLAPARPRGPLICHTGHEQA GREPGGSST  
 KGPVLHDQDTRCAFLPRPPGPLQTRRYCRHQGRQSGLGAGPGAGTWAPPGVSKPRCPGRARPGEGQQQVTTARPPAIN  
 RGARQPRAGAAAGRPGGAGAWRTGEAAASAGPAVGGGAMGSRRAPTRGWAGGRSGAGGDGEDDGPVWIPSPASRS  
 YLLSVRPETSLSSNRLSHPPSSGRSTFCIIIAQLTEETQPLFETTLKRSVSESDSVRFTCIVTGYPEPEVTWYKDDDELDRYCGL  
 PKYEITHQGNRHTLQLYRCREEDAIIYQASAQNSKGIVSCSGVLEVTMEYKIHQRWFAKLKRKAAAKLREIEQSWKHEK  
 AVPGEVDTLRKLSRDRFORRRRLSGAQAPGPSVPTREPEGGLAAWQEGETETAQHSLGLINSFASGEVTTNGEAAAPENGE  
 DGEHGLLTYICDAMELGPQRALKEESGAKKKKDEESKQGLRKPELEKAAQSRSSENCIPSSDEPDSCGTQGPVGVQVQT  
 QPRGRAARGPGSSGTDSTRKPPASAVGTPDKAQKAPGPGQEVYFSLKDMYLENTQAVRPLGEEGPQTL SVRAPGESPKGK  
 APLRARSEGVPGAPGQPTHSLTPQPTRPFNRKRFAPPKPKGEATTDSKPISLSQAPECGAQSLGKAPPQASVQVPTPARRRH  
 GTRDSTLQQAQHRTPGEVLECQTTTAPTMSASSSDVASIGVSTSGSQGHIIEPMDMETQEDGRTSANQRTGSKKNVQADGK  
 IQVDGRTRGDGTQTAQRTRADRKTDVDAQTQESKRPQSDRSQAQKGMMTQGRAETQLETTQAGEKIQEDRKAQADKGTQE  
 DRRMQGEKGMQGEKGTQSEGSAPTAMEGQSEQEVATSLGPPSRTPKLPPTAGPRAPLNIECFVQTPEGSCFPKPGCLPRSEE  
 AVVTASRNHEQTVLGPLSGNLM LPAQPPHEGSVEQVGGERCGRGPQSSGPVEAKQEDSPFQCPKEERP GGVPVPCMDQGGCPLA  
 GLSQEVPTMPSLPGTGLTASPKAGPCSTPTSTQHGSTATFLPSEDQVLMSSAPTLHLGLGTPTQSHPPETMATSEGACACQVPD  
 VEGRTPGPRSCDPPGLIDSLKNYLLLLKLSSTETSGAGGESQVGAATGGLVPSATLTPTTVEVAGLSRPTSRRLERVENNHLV  
 QSAQTL LLSPTCSRRLTGLLDREVQAGRQALAAARGSWGPGPSSLTVP AIVVDEEDPGLASEGASEGEVSLGPGLLGAS  
 QESSMAGRLGEAGQAAPGQGPSAESIAQEPSQEEKFPGEALTGLPAATPEELALGARRRKFLPKVRAAGDGEATTPEERES  
 PTVSPRGRKSLVPGSPGTPGRRRSPTQGRKASMLEVPRAEELAAAGDLGPSKAGGLDTEVALDEGKETLAKPRKAKDL  
 LKAPQVIRKIRVEQFPDASGSLKLWCQFFNILSDSVLTWAKDQRPVGEVGRSAGDEGPAALAIVQASPVDCGVYRCTIHNEH  
 GSASTDFCLSPVLSGFISREEGEVGEEIEMTPMVFAKGLADSGCWGDKLFGRLVSEELRGGYGCGGLRKASQAKVIYGLEPI  
 FESGRTCIIKVSSLLVFGPSSSETSLVGRNYDVTTQGCKIQNMSREYCKIFAAEARAAPGFGEVPEIPLYL IYRPANNIPYATLEE  
 DLGKPLESYCSREWGC AEAPTASGSSEAMQKCTFQHWLYQWNTNGSFLVTDLAGVDWKMTDVQIATKLRGYQGLKESCF  
 PALLDRFASHQCNA YCELLGLTPLKGPEAAHPQAKAKGSKSPSAGRKGSQLSPPQKKGLPSPQGT RKSAPSSKATPQASEP  
 VTTQLLGQPPTQEEGSKAQGM R

Figure 10B

ATGAATAATCAAAAAGTGGTAGCTGTGCTACTGCAAGAGTGCAAGCAAGTGCATCAGCTCTTTGTAAGCGCCAGATGTGTGCGGAAGAGGACAAGAGCGGA  
GGACCAGCGCTGCAGAGCTTTACTTCCCCAGGAGTTAAGGACCCTGTATCCAGGAGGCAAGGAAATGAAGTGGCCCTTCGTGCTGAAAAGTGGCAGTACAAAC  
AAGCGTGGGCCGACAGGACAAACAACCTGAAGGATGTGATTTGGCGCCGGTTCGACGAGTTACTGGCTCCCTGAGGGCTCCATCCTCGCTCGGACTGT  
CGGCTGGCGGCTATTTGTGTTCTTGGTGGACCGGTTCCTGTATGGCTCGACGTCTCTGAAAACCTTCTGCAAGTCCGCAAAAGTTCACAAAGTTCGACGCCAG  
CCACGCCAATTGCCCGCAGGTGTTATTTCGCCAACCCGGAATCTCCGTGAATCTCAGGAAACCTTTAAAGCAGAGTATATTCTGAGCAGTCTAATAAGCAACA  
ATGGAGCAACGGGTACCTGGCTGTACAGAAATGAAGGTGACAAGTTCTGGTCAGTGGTGTATACAGATCAGAGGGCAGATTTCTGCAAAAGTGGGTATG  
TGGTACGAAGCAGCAGAGTTAATATATGGGCTCCATTTGAGGATTTGAGGATTTGAGGCTCTGTAAGGAGTTTGACCAACCATTTGCTGCTCCGCTGCAG  
ATCTTTGTTTCCA'GAGCAAGAACGAT'ATGAAAAGT'IT'AAAAAACAATCCACAAT'AAATTTGAGCCTCTGAAGGAGTTTGACCAACCATTTGCTGCTCCGCTGCAG  
AAGCCTGCAAGCTGGCAGCTGCCTTCAGTGGCT'ATACGCCGCTCTCTG'GCTCACAGCTGTGAATATCCGTGGCACGTGTTATTGTCTCACAGTATGTTCAAAATGA  
GTCTTCCAGAAIT'GAAAACCTTACA'CT'GIGTGAAGCCAAAGAGGCCCTTTGAGATTTGGCTCTCTCACCAAGAGAGATGATGAGCCTGT'ACTGGAACAACAGGA  
CCTTCCACAGCTTTG'CAAAAGCTGCTTCCGTCTCACCAAGTGCACAGAAAGGCTCCATGGGGAGACAGGAGGTCCAT'GCGCAAGTCAAGCTCTGTTAAAGGAAGC  
AATGGGAAGCTGTACAAITTCAGCACTTCTCCAGAACTCAGGACAGAGAAAGTCTCTGTCAAGAGAT'ATGTTCTGATGGCAAGGGAATTTCCCAAAAAT  
AGTTCAAAGCTTCTCAAATGTAGATGACAGAT'CT'ATGTTCCCGAGAGT'ITCGAGTGCAGGTGTGATAAACT'ATCTGATGGCAAGGGAATTTCCCAAAAAT  
CCTTGACACCTA'TTCACAGCACCATACTTCGGTGTGTGAAGTATTTGAAAGTGA'ITGTGGAACAACAACAAAT'GAA'CAAGAAAGATGCAAAAACAGGAGTCTGCA  
TCACTGCT'ATAAAAACAGAAAT'AAAAACAATAGATACTGTGAGTACTACTCAAGAAAAGCCACATTTGTCAAAGAGACACAGGAATATCTTCTCCCTAATGGGT  
AAGATTTTCAGAGGAACTCAGAAAGGGGAGGAGGAAACTGACCCCA'CTCTGATGCAITTCGAGTCTCTTGATCAAGATGTGAGAGCTGAGACTGAGCGTGA  
ATCGGACTACAGCAATTTGGTGGAGGAGCTTTTCAACAAGTCTGTGATGGCAGCCAGACTTCCAGTCTTGAGACCACTTATCAGGGTGTAGTTCTCTGCAAG  
CTGGGAGGAAGTGAAT'ATACGTTTGACGACAGTTCAGCCAGAAAAGAGCTGGCAAGAAACATCTGGTGACACTCAGTGTCCACTTCTGCTGAGGAG  
TAGAGAATGACAGGGAAGGCAGAGCTATGCAITTCATTTGCATTCACAGCTTCATGATCTCTCTTCAGGAACCAACAATGACAATTTGAGAGCTTCTCAAAATC  
AGCCAAGCAACAGATGCCCTTGACACCCCTCTCGCCTCATATAACCCAGGCATTTTCTTGGCCCTGGTGCAGGGCTCTAGAAAGGAGCTCCAGAAAGGTATCC  
AGGAAGTCAAAATATGGGACCCAGAAATACTTGTCTCACTCCAGACCCCTCATATGCTTCTGTTCTGTTCTGATTTCTGTTAGGCCCAAGAATATGGGCAC  
ACATCTTCAGTCCAAAAGAAAGAGCTTTGAATAATTTGTGAGTTTCCAGAAACCAACTGCGATGTCAAAGACAGCGGGAAGAGCAGGGAAGAA  
A'ITAGTGAAGAGCGCAGCCCTACATTTAAAGCTAGTCCCTCTGGTTGACCCAGAAAGGAACACAGCAGCAAGCACTGAAGATGACACCTTAGACTTCA  
CAGGCTCTGCACAAATCTCTGGGAAACA'ITTTCCATGTGTGCCATGTAGCTCTTCAACCCATAATTTGGCCTGTTCAAAATCTGACTCCAGAAAAGTGGTGGCCCA  
GTGCAAGCAGGGCATCGACCTGATGCC'TCCACAGTGGATGAGGAGGGCAACTGCTCGACAGCATGGATGTTCCTTCGCAAAAATGGGCAAGGCTCTCATAG  
ACTGTGCATTTGAGACAGCCGCTGTGAGAGGGGAGACCCCAATTCCTCTGTAAAGCGTAACTCTCTTCCCTGTCTCAGCGAGGAGCTGCACCTACCAC  
AGGGAAGGAAATTCAGCCTGAAACATGTCTAACTGACAGCAGAACTCCAGCTCATCTCAGTGTGGTGGCTGAATAACACTGCTTTCAGGGCTCGCACTTCTGTA  
GGGGAGAGCCCTTGTGCTATCTGAATTCAGTGGGAGTTC'TTGGGTTTCAATTCGGGAAAGATGAGGAAGAGATCC'TTGGAGGCTCGCACTTGCACAACTGTGA  
TGACTTTGAAAAGCTGTGGCAGGATGAGGCATGATTGGCTGTTCAGAGACTAGAGAAATACGGGGTTTTTAAAGCCAGTCAACTCCACCGACACATATGTC  
TCTTTTGTAAATATTCAAAANAATCTGAACTGTGGAACGGCCAGGAAACTATTTGCTATTTTGGGGACTACTTGAAGTGAAGAAAAGGACAGACAAAAGAA  
TGTCTTTTGGGTTTCATCTCTCATCAAGAAAGAAATCTGGGAGGTA'ITGTGGAAAGACTATAAGGAGCAGAAAGGGGCTCTGGCACCACTTCACTGATGTGGA  
GGCAGAGATGACCGCAGCACTATGTGACAGAAATTAACAAGAGACTCTATGAACAAAACATTCACCCACAGATATCTACATCCCATCCACAATACTACTGAT  
TTAGGAGCAAGACAAATAAGGAGTGTATCAGTGTGGAGCCTTACATCTGGAGGAAATTTGTAAAAATGTCAAA'TAACACGAAAGTGGTGAACACAGAAATACA  
AAGCACAGAAATATGGCTTGGCCTATGGCCATTTTCTTATGAGTTTCTAATCATAGAGATGTTGTGGTGCATTTACAAGTGTGGTAACCGGTAATGGAAAAGG  
ACTCATCTACCTCACAGATCCCAAGATTCACCTCCGTGTATCAGAAAAGTTTCACTACCAATTTTGGAAAGAGAGGAATTTTCTTCTTAAATAACCCAGCATGTG  
GAATGTAATGAAATCTGCCATCGTCTTTCTTTGACTAGACCTTCAATGGAGAAAACCA

**Figure 11A**

MNNQKVAVLLQECKQVLDQLLEAPDVSEEDKSEDQRCRALPSELRTLIQEAEMKWPFVPEKWQY  
 KQAVGPEDKTNLKDVGAGLQQLLASLRASILARDCAAAAIIVFLVDRFLYGLDVSGKLLQVAKGLHKL  
 QPATPIAPQVVIRQARISVNSGKLLKAEYILSSLISNNGATGTWLVRNESDKVLVQSVCIQIRGQILQKLG  
 WYEAELIWAIVGYLALPQPDKKGLSTSLGILADIFVSMKNDYEKFKNNPQINLSLKEFDHLLSAAE  
 ACKLAAAFSAITPLFVLTAVNIRGTCLLSYSSNDCPPELKNLHLCEAKEAFEIGLLTKRDDDEPVTGKQEL  
 HSFVKAAGLTTVHRRLLHGETGVHAASQLCKEAMGKLYNFSTSSRSQDREALSQEVMMSVIAQVKEHLQ  
 VQSFNSVDDRSYVPESFECRLDKLILHGQGFQKILDY'SQHHTSVCEVFESDCGNNKNEQKDAKTGVCI  
 TALKTEIKNIDTVSTTQEKPHCQRTGISSSLMGKNVQRELRRGGRNWTHTSDAFRVSLDQDVETETEPSD  
 YSNGEGA VFNKSLSGSQTSASWSNLGFSASWEEVNYHVDDRSARKEPGKEHL VDTQCSTALSELEN  
 DREGRAMHSLHSLHDLSLQEPNNDNLEPSQNQQQMPLTPFSPHNTPGIFLAPGAGLLEGAPEGIQEVR  
 NMGPRNTSAHSRPSYRSASWSSDSGRPKNMGTSPVQKEEAFEIIVEFPETNCDVKDRQGKEQGEEISERG  
 AGPTFKASPSWVDPEGETAESTEDAPLDFHRVLHNSLGNISMLPCSSFTPNWPVQNPDSRKSGGPVAEQGI  
 DPDASTVDEEGQLLDSDMDVPCTNGHSHRLCILRQPPQRAETPNSSVSGNILFPVLSLSEDCCTTTEEGNQPG  
 NMLNCSQNSSSSVWWLKSPAFSSGSSEGDSPWSYLNSSGSSWVSLPGKMRKEILEARTLQPDDEFKLLA  
 GVRHDWLFQRLNTGVFKPSQLHRAHSALLKYSKKSELWTAQETIVYLG DYLT VKKKGRQRNAFWVH  
 HLHQEEILGRYVGKDYKEQKGLWHHFTDVERQMTAQHYVTEFNKRLYEQNIPQTQIFYPSTILLILEDKTIK  
 GCISVEPYILGEFVKLSNNTKVVKTEYKATEYGLAYGHFSYEFNSHRDVVVDLQGWVTGNGKGLIYLTDP  
 QIHSVDQKVFTTNFGKRGIFYFFNNQHVCECHRLSLTRPSMEKP

Figure 11B

HeEF-2\_kinase> 1 LDD--EQLKCAQPPGR-----EYECSTKESNFLHAQQWKGASN--AARRIEPDR---DVF  
 MHCK\_B> 1 ECT--ATLAKSEFPVFAD-----EFTLETLDS-----KSGASGR--SIGKKPTPR---PSRP  
 Melanoma\_kinase> 1 QGLGLCAKSEFLDQEMG-----EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Kidney\_kinase> 1 SGRGRAAGSGLRQEMD-----EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Muscle\_kinase> 1 GDK--EFGRTVDELRG--GYGCC--SQAKVHYG--LEPNFESRTCH--VSSLL--PGPSSSETSLVGRNYDTIQG  
 Heart\_kinase> 1 RGR--EFGRTVDELRG--GYGCC--SQAKVHYG--LEPNFESRTCH--VSSLL--PGPSSSETSLVGRNYDTIQG  
 Lymphocyte\_kinase> 1 QAQETISVIGDYLTIVKKK-----RCNLEWVHHSH-----QEEILGR--GDDKQKGL---WHHFT  
 consensus 1 vt v im se G amRkafr l i g yvik y v y ed 1

HeEF-2\_kinase> 62 YRDMEERLGGSETRH--PKQ--VDTMOYCIHE--KDP--GKPLSH--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 MHCK\_B> 56 EKI--MI--KADK--SF--PKK--IEFLQSCVSEFPDST--SSDLICG--AP--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Melanoma\_kinase> 74 HCO--RA--QALTF--QM--EKSI--FYS--RFLDEE--EYCH--SAGQAP--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Kidney\_kinase> 74 HCO--RA--QALTF--QM--EKSI--FYS--RFLDEE--EYCH--SAGQAP--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Muscle\_kinase> 75 CK--NM--SEYCKI--AAEARAAPGFGV--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Heart\_kinase> 73 CY--NT--EYAKI--AAEQAQFLGFGV--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Lymphocyte\_kinase> 58 YER--MT--QHLVTE--KRLYSQNIPTQ--FYSPSTI--ELEDKTKIGCIS--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 consensus 81 v lQ akkw fn kp dip al iflv r f lB yi gef kynnn g v dt

HeEF-2\_kinase> 130 LTPQ--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 MHCK\_B> 124 NTPQ--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Melanoma\_kinase> 145 EIML--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Kidney\_kinase> 145 EIML--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Muscle\_kinase> 154 QKCT--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Heart\_kinase> 150 QKCT--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 Lymphocyte\_kinase> 132 EYGL--EYVQVQCTNS--EHDLLKSHL--SSLPK--VMTWSSIK--TVLRLCLRE  
 consensus 161 afsRwtyeyt g llvDlqG vg d lTdpqi t d g fg gnlg gm F H CN C

HeEF-2\_kinase> 196 ESE--G--APP  
 MHCK\_B> 190 QY--N--QS  
 Melanoma\_kinase> 216 EKK--K--PDR  
 Kidney\_kinase> 216 EKK--K--PDR  
 Muscle\_kinase> 221 EL--G--TP  
 Heart\_kinase> 217 EKK--K--PDR  
 Lymphocyte\_kinase> 206 ERS--S--TRP  
 consensus 241 r l L i

HEEF-2\_kinase> 196 ESE--G--APP  
 MHCK\_B> 190 QY--N--QS  
 Melanoma\_kinase> 216 EKK--K--PDR  
 Kidney\_kinase> 216 EKK--K--PDR  
 Muscle\_kinase> 221 EL--G--TP  
 Heart\_kinase> 217 EKK--K--PDR  
 Lymphocyte\_kinase> 206 ERS--S--TRP  
 consensus 241 r l L i

# PHYLOGENETIC TREE OF ALPHA-KINASES

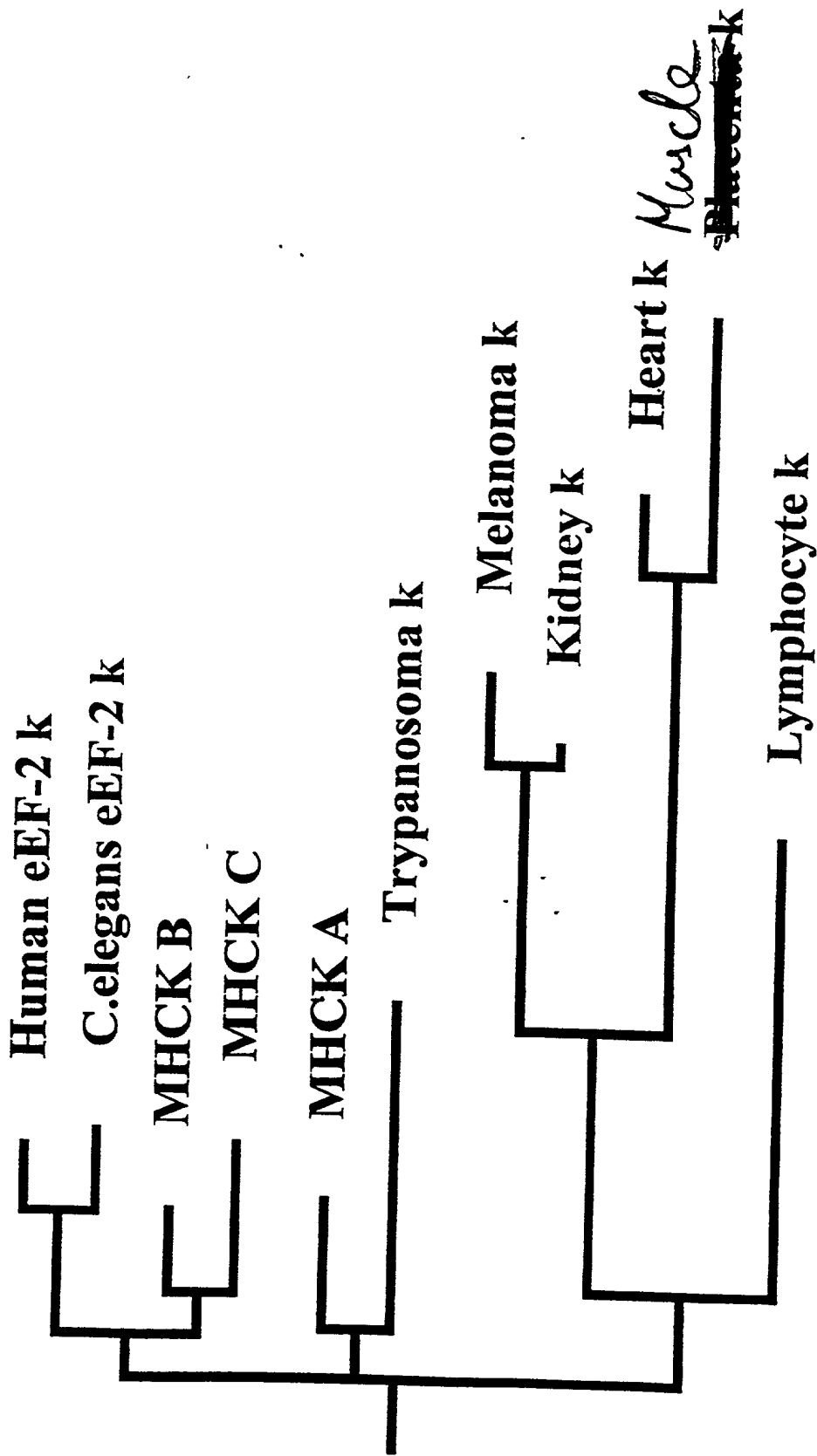


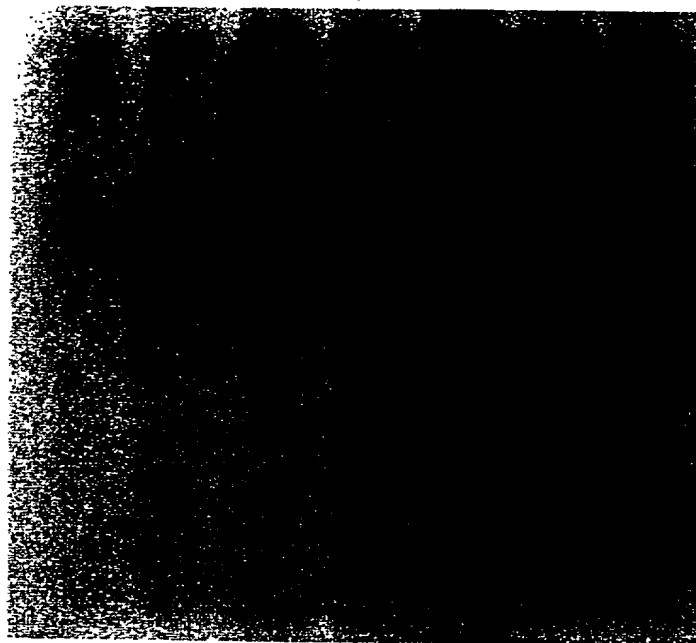
FIGURE 13

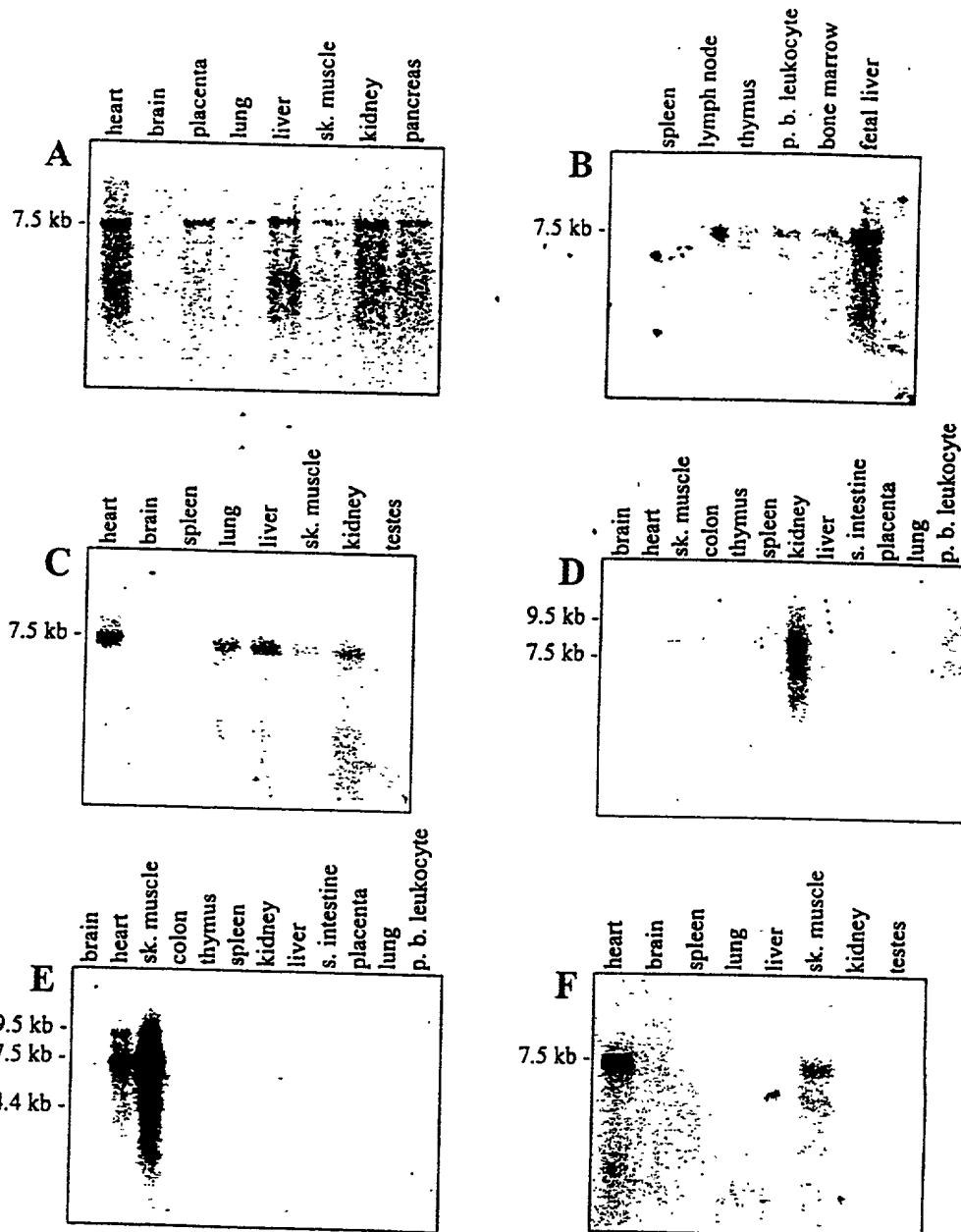


Time curve

melanoma kinase  
catalytic domain.

0' 5' 10' 20' 30' 60' 120'





[illegible][illegible]

Figure 17

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MELANOMA\_KINASE> 551  
KIDNEY\_KINASE> 552  
LTPC4\_NTR1\_> 553  
LTPC4> 554  
MELANOSTATIN> 555  
LTPC4\_TRPC\_> 556  
DMLTRPC> 557  
CALTRPC> 558  
CALTRPC2> 559

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KIDNEY\_KINASE> 561  
LTPC4\_NTR1\_> 562  
LTPC4> 563  
MELANOSTATIN> 564  
LTPC4\_TRPC\_> 565  
DMLTRPC> 566  
CALTRPC> 567  
CALTRPC2> 568

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KIDNEY\_KINASE> 570  
LTPC4\_NTR1\_> 571  
LTPC4> 572  
MELANOSTATIN> 573  
LTPC4\_TRPC\_> 574  
DMLTRPC> 575  
CALTRPC> 576  
CALTRPC2> 577

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LTPC4\_TRPC\_> 583  
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KIDNEY\_KINASE> 588  
LTPC4\_NTR1\_> 589  
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CALTRPC> 594  
CALTRPC2> 595

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MELANOSTATIN> 627  
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CALTRPC2> 649

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KIDNEY\_KINASE> 651  
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KIDNEY\_KINASE> 660  
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LTPC4\_TRPC\_> 952  
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CALTRPC> 954  
CALTRPC2> 955

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CALTRPC2> 973

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KIDNEY\_KINASE> 993  
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CALTRPC> 999  
CALTRPC2> 1000

Figure 17

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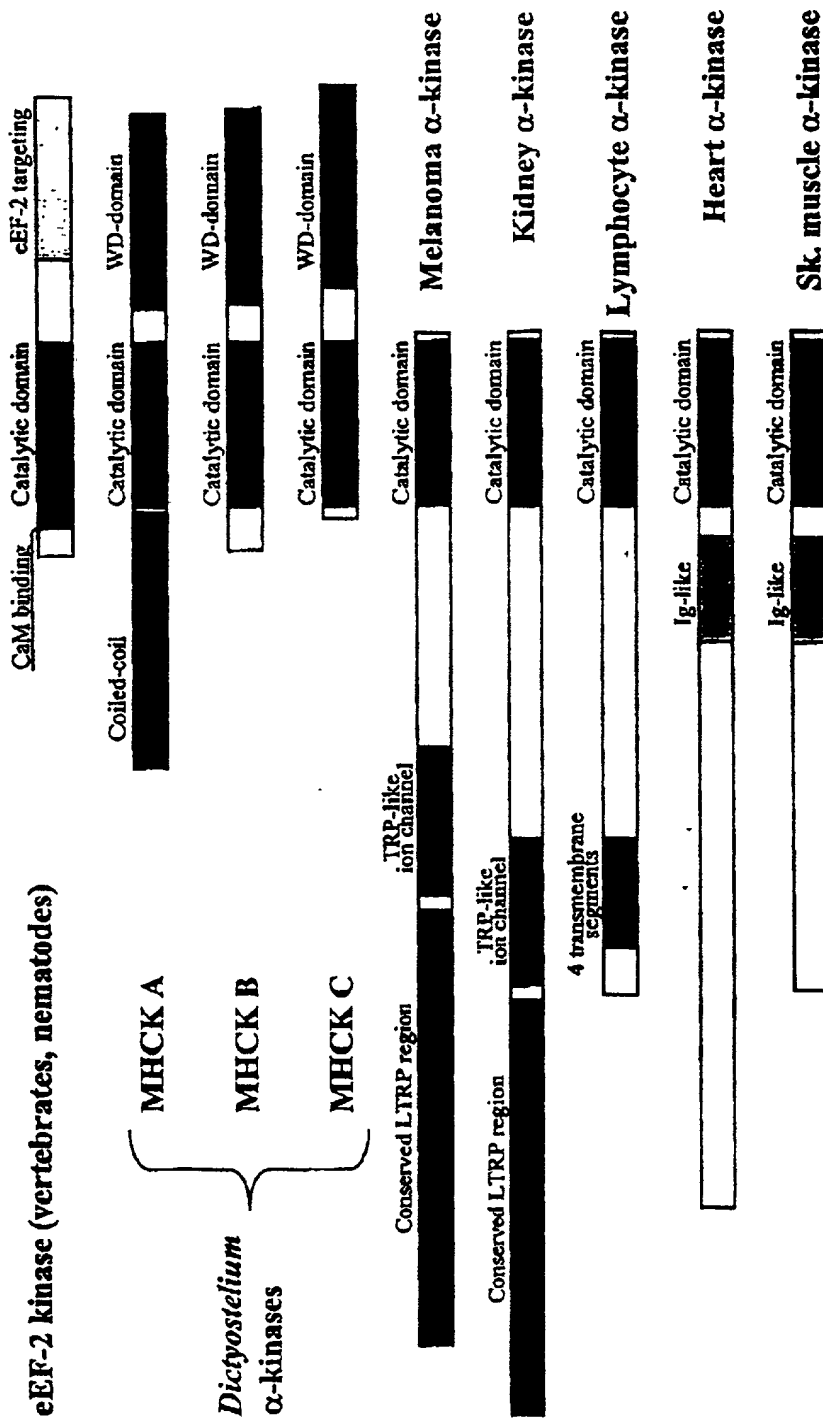


Figure 18

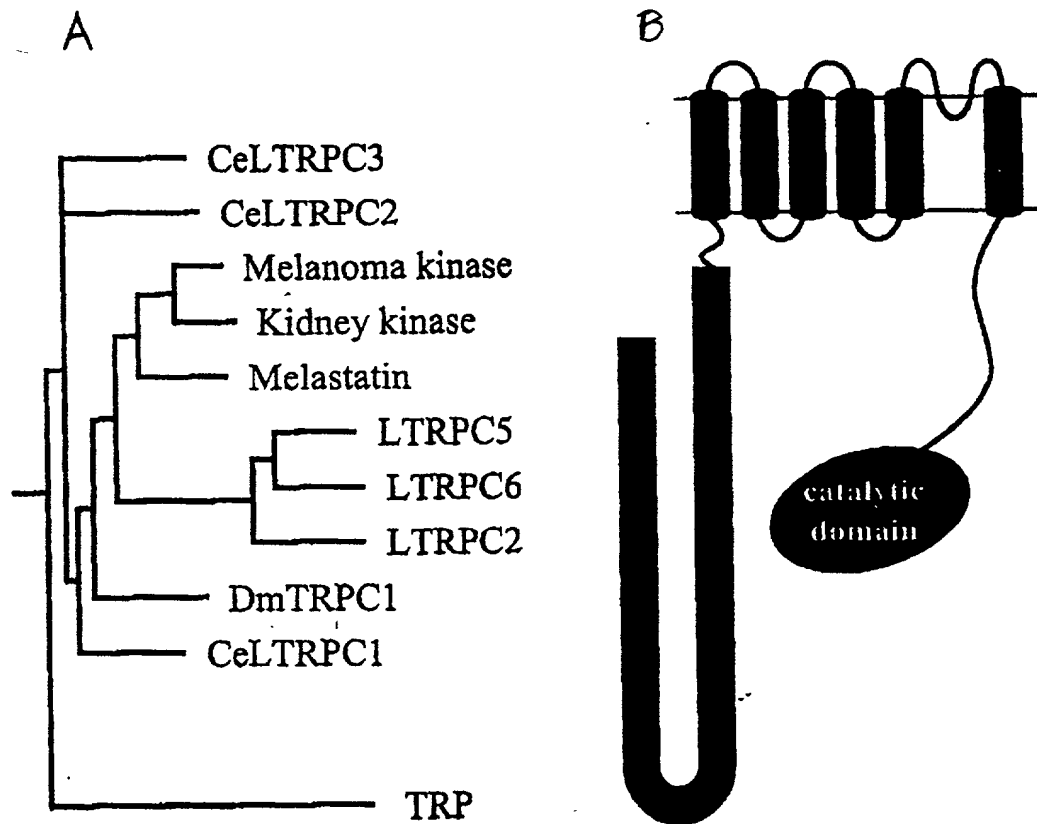


Figure 19A&B